

ABSTRACT

The present invention applies classical survival analysis to genome-wide gene expression profiles of prostate cancers and preoperative prostate-specific antigen levels from prostate cancer patient, to identify prognostic markers of disease relapse that provide additional predictive value
5 relative to prostate-specific antigen concentration. The present invention provides a method of determining prognosis of prostate cancer and predicting prostate cancer outcome of a patient. The method comprises the steps of first establishing the threshold value of at least one prognostic gene of prostate cancer. Then, the amount of the prognostic gene from a prostate tissue of a prostate cancer patient is determined. The amount of the prognostic gene present in
10 that patient is compared with the established threshold value of the prognostic gene, whereby the prognostic outcome of the patient is determined.